In the Claims

Please amend the following claims according to the following listing of claims under 37 CFR 1.121.

Listing of Claims under 37 CFR 1.121:

We claim:

1-90 (CANCELED)

91. (CURRENTLY AMENDED): A composition for use in obtaining genotype data or sample allele frequency data, comprising: one or more copies of a set of oligonucleotides, the set of oligonucleotides being complementary to a group of two or more bi-allelic covering markers, wherein the set of oligonucleotides is selected for the set's utility to determine genotype data or sample allele frequency data for each of the two or more covering markers, wherein the group of covering markers is chosen so that a CL-F region is N covered to within [x, y] by the covering markers, wherein [x, y] is a two-dimensional distance, wherein x is less than or equal to 1 million base pairs and y is less than or equal to 0.2, N is an integer greater than or equal to 1, the covering markers and the CL-F region being for a species of creatures, the CL-F region being a collection of one or more points on a two-dimensional CL-F map that is similar to an x-y graph, the CL-F map having the two orthogonal dimensions of chromosomal location (CL) and least common allele frequency (F), whereby each point in the region is within the distance [x, y] of each of N or more of the covering markers,

wherein the CL-F region is a segment-subrange, whereby the segment-subrange is a rectangular region on the CL-F map, whereby the segment-subrange is bounded by a chromosomal segment and a least common allele frequency subrange, wherein the length of the segment of the segment-subrange is greater than or equal to the length of human chromosome 21, ~~whereby the length of the segment is greater than or equal to about 47 million base pairs,~~ wherein the subrange of the segment-subrange includes the least common allele frequency 0.1,

~~whereby there are at least about 24 covering markers with least common allele frequencies less than or equal to 0.3 that are distributed within the segment with a density of at least about 1 marker every two million base pairs~~.

92. (PREVIOUSLY ADDED): A composition as in claim 91, wherein the CL-F region is for the species of creatures and for a population, wherein the population is a population as in the field of population genetics and wherein each covering marker is an SNP.

93-104 (CANCELED)

105. (CURRENTLY AMENDED): A composition as in claim 92, wherein the subrange of the segment-subrange is the subrange 0 to 0.1, wherein N is greater than 2, ~~whereby there are at least about 288 covering markers with least common allele frequencies less than or equal to 0.2 that are distributed within the segment with a density of at least about 1 marker every 167 thousand base pairs~~.

106-211 (CANCELED)

212. (PREVIOUSLY ADDED): A composition as in claim 105, wherein each oligonucleotide in the set is a type (1) complementary oligonucleotide that is allele specific or wherein each oligonucleotide in the set has utility as a polymerase chain reaction primer-and the composition has utility to obtain genotype data or sample allele frequency data by generating a signal, wherein the signal is generated by the products of a polymerase chain reaction when oligonucleotides of the composition hybridize with one or more complementary alleles of one or more of the covering markers.

213-235 (CANCELED)

236-307. (WITHDRAWN)